

RESULT 1
Y938_MYCTU
ID Y938_MYCTU Reviewed; 759 AA.
AC P71571; 005865;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 30-MAY-2000, sequence version 2.
DT 24-NOV-2009, entry version 67.
DE RecName: Full=Putative DNA ligase-like protein Rv0938/MT0965;
GN OrderedLocusNames=Rv0938, MT0965; ORFNames=MTCY08D9.01c, MTCY10D7.36c;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 25618 / H37Rv;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eigmleier K., Gas S., Barry C.E. III,
RA Tekaiwa F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
CC !- SIMILARITY: Belongs to the ATP-dependent DNA ligase family.
CC -----
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CC -----
DR EMBL; BX842575; CAB08492.1; -; Genomic_DNA.
DR EMBL; AE000516; AAK45212.1; -; Genomic_DNA.
DR PIR; B70585; B70585.
DR RefSeq; NP_215453.1; -.
DR RefSeq; NP_335398.1; -.
DR PDB; 1VS0; X-ray; 2.40 Å; A/B=452-759.
DR PDB; 2IRU; X-ray; 1.65 Å; A/B=1-300.
DR PDB; 2IRX; X-ray; 1.80 Å; A=1-300.
DR PDB; 2IRY; X-ray; 1.78 Å; A/B=1-300.

DR PDB; 2R9L; X-ray; 2.40 Å; A/B=1-300.
 DR PDBsum; 1V50; -.
 DR PDBsum; 2IRU; -.
 DR PDBsum; 2IRX; -.
 DR PDBsum; 2IRY; -.
 DR PDBsum; 2R9L; -.
 DR GeneID; 885561; -.
 DR GeneID; 926354; -.
 DR GenomeReviews; AE000516_GR; MT0965.
 DR GenomeReviews; AL123456_GR; Rv0938.
 DR KEGG; mtc:MT0965; -.
 DR KEGG; mtu:Rv0938; -.
 DR TIGR; MT0965; -.
 DR TubercuList; Rv0938; -.
 DR HOGENOM; P71571; -.
 DR OMA; VDWSQNN; -.
 DR GO; GO:0005524; F:ATP binding; IEA:UniProtKB-KW.
 DR GO; GO:0003910; F:DNA ligase (ATP) activity; IEA:InterPro.
 DR GO; GO:0003896; F:DNA primase activity; IEA:InterPro.
 DR GO; GO:0006310; P:DNA recombination; IEA:InterPro.
 DR GO; GO:0006281; P:DNA repair; IEA:InterPro.
 DR GO; GO:0006269; P:DNA replication, synthesis of RNA primer; IEA:InterPro.
 DR InterPro; IPR012309; DNA_ligase_A_C.
 DR InterPro; IPR012310; DNA_ligase_A_M.
 DR InterPro; IPR002755; DNA_primase_S.
 DR InterPro; IPR014144; LigD_PE_domain.
 DR InterPro; IPR014145; LigD_pol.
 DR InterPro; IPR012340; NA_bd_OB-fold.
 DR InterPro; IPR014146; NHEJ_ligase_lig.
 DR Gene3D; G3DSA:2.40.50.140; OB_NA_bd_sub; 1.
 DR Pfam; PF04679; DNA_ligase_A_C; 1.
 DR Pfam; PF01068; DNA_ligase_A_M; 1.
 DR Pfam; PF01896; DNA_primase_S; 1.
 DR TIGRFAMs; TIGR02777; LigD_PE_dom; 1.
 DR TIGRFAMs; TIGR02778; ligD_pol; 1.
 DR TIGRFAMs; TIGR02779; NHEJ_ligase_lig; 1.
 DR PROSITE; PS50160; DNA_LIGASE_A3; 1.
 PE 1: Evidence at protein level;
 KW 3D-structure; ATP-binding; Complete proteome; Ligase;
 KW Nucleotide-binding.
 FT CHAIN 1 759 Putative DNA ligase-like protein
 FT Rv0938/MT0965.
 FT /FTId=PRO_0000059627.
 FT ACT_SITE 481 481 N6-AMP-lysine intermediate (By
 FT similarity).
 C -> R (in Ref. 2; AAK45212).
 FT CONFLICT 344 344
 FT TURN 20 22
 FT HELIX 26 44
 FT STRAND 50 53
 FT STRAND 63 65
 FT STRAND 76 83
 FT STRAND 86 92
 FT HELIX 96 104
 FT STRAND 109 112
 FT STRAND 114 119
 FT TURN 121 123
 FT STRAND 126 140

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FT  HELIX      146  162
FT  STRAND     168  171
FT  STRAND     173  175
FT  STRAND     177  187
FT  HELIX      189  206
FT  TURN       208  210
FT  HELIX      217  219
FT  STRAND     221  227
FT  HELIX      229  231
FT  STRAND     246  248
FT  HELIX      257  260
FT  HELIX      270  280
FT  TURN       283  290
FT  HELIX      455  457
FT  STRAND     462  465
FT  TURN       473  475
FT  STRAND     476  479
FT  STRAND     484  492
FT  STRAND     495  500
FT  HELIX      507  509
FT  HELIX      511  513
FT  HELIX      514  519
FT  TURN       520  522
FT  STRAND     524  532
FT  HELIX      542  546
FT  STRAND     555  564
FT  HELIX      574  587
FT  HELIX      600  609
FT  STRAND     614  619
FT  STRAND     629  650
FT  STRAND     662  669
FT  STRAND     672  679
FT  HELIX      685  695
FT  HELIX      696  698
FT  STRAND     704  707
FT  HELIX      711  714
FT  STRAND     717  720
FT  STRAND     725  731
FT  STRAND     743  747
FT  HELIX      753  755
SQ  SEQUENCE   759 AA;  83572 MW;  81BD49222EE09E36 CRC64;
Query Match          100.0%;  Score 3993;  DB 1;  Length 759;
Best Local Similarity 100.0%;
Matches 759;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy          1 MGSASEQRVTLNADKVLYPATGTTKSDIFDYYAGVAEVMLGHIAGRPATRKRPNGVQDQ 60
           |||||||...|||||...|||||...|||||...|||||...|||||...|||||...|||||...|||
Db          1 MGSASEQRVTLNADKVLYPATGTTKSDIFDYYAGVAEVMLGHIAGRPATRKRPNGVQDQ 60
           |||||||...|||||...|||||...|||||...|||||...|||||...|||||...|||||...|||
Qy          61 PAFFEKQLALSAPPWLSRATVAHRSGTTTYPIDIISATGLAWIAQQAALEVHVPQWRFAE 120
           |||||||...|||||...|||||...|||||...|||||...|||||...|||||...|||||...|||
Db          61 PAFFEKQLALSAPPWLSRATVAHRSGTTTYPIDIISATGLAWIAQQAALEVHVPQWRFAE 120
           |||||||...|||||...|||||...|||||...|||||...|||||...|||||...|||||...|||
Qy          121 PGSGELNPGPATRLVFLDDPGEVGVMMAQALAEVARAVRDLRADIGLVTFPVTSGSKGLHLY 180
           |||||||...|||||...|||||...|||||...|||||...|||||...|||||...|||||...|||
Db          121 PGSGELNPGPATRLVFLDDPGEVGVMMAQALAEVARAVRDLRADIGLVTFPVTSGSKGLHLY 180
           |||||||...|||||...|||||...|||||...|||||...|||||...|||||...|||||...|||

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Qy	181	TPLDEPVSSRGATVLAKRVAQRLEQAMPALVTSTMKSRLAGKVFDWSQNSGSKTTIAP	240
Db	181	TPLDEPVSSRGATVLAKRVAQRLEQAMPALVTSTMKSRLAGKVFDWSQNSGSKTTIAP	240
Qy	241	YSLRGRTHPTVAAAPRTWAELDDPALRQLSYDEVLTRIARDGDLLERLDADAPVADRLTRY	300
Db	241	YSLRGRTHPTVAAAPRTWAELDDPALRQLSYDEVLTRIARDGDLLERLDADAPVADRLTRY	300
Qy	301	RRMRDASKTPEPIPTAKPTVGDGNTFVIQEHHARRPHYDFRLECDGVLVSWAVPKNLPDN	360
Db	301	RRMRDASKTPEPIPTAKPTVGDGNTFVIQEHHARRPHYDFRLECDGVLVSWAVPKNLPDN	360
Qy	361	TSVNHLAINTEDHPLEYATFEGAIPSGEYAGKVIWDSGTYDTEKFHDPPHTGEIVVN	420
Db	361	TSVNHLAINTEDHPLEYATFEGAIPSGEYAGKVIWDSGTYDTEKFHDPPHTGEIVVN	420
Qy	421	HGGRISGRYALIRTNQDRWLAHRLKNQKDQVFEFDNLAPMLATHGTVAGLKASQWAFEG	480
Db	421	HGGRISGRYALIRTNQDRWLAHRLKNQKDQVFEFDNLAPMLATHGTVAGLKASQWAFEG	480
Qy	481	KWDGYRLLVEADHGAVRRLRSRSGRDVTAEYPQLRALAEDLADHHVVLGEAVVLDSSGVP	540
Db	481	KWDGYRLLVEADHGAVRRLRSRSGRDVTAEYPQLRALAEDLADHHVVLGEAVVLDSSGVP	540
Qy	541	SFSQMQNRRGDRTRVEFWAFDLYLDGRALLGTRYQDRRKLETLTANATSLTVPELLPGDG	600
Db	541	SFSQMQNRRGDRTRVEFWAFDLYLDGRALLGTRYQDRRKLETLTANATSLTVPELLPGDG	600
Qy	601	AQAFACSRKHGWEGVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWRAGEGGRSSGV	660
Db	601	AQAFACSRKHGWEGVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWRAGEGGRSSGV	660
Qy	661	GSLLMGIPGPGLQFAGRVTGLSERELANLKEMLAPLHTDESPFDVPLPARDAKGITYV	720
Db	661	GSLLMGIPGPGLQFAGRVTGLSERELANLKEMLAPLHTDESPFDVPLPARDAKGITYV	720
Qy	721	KPALVAEVRYSEWTPEGRLRQSSWRGLRPDKKPSEVVRE	759
Db	721	KPALVAEVRYSEWTPEGRLRQSSWRGLRPDKKPSEVVRE	759

RESULT 1

B70585

hypothetical protein Rv0938 - *Mycobacterium tuberculosis* (strain H37RV)

C;Species: *Mycobacterium tuberculosis*

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: B70585

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Teknia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537–544, 1998

A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70585
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-759
A;Cross-references: UNIPROT:P71571; UNIPARC:UPI0000139E3C; GB:Z95209; GB:AL123456;
NID:g3261750; PIDN:CA08492.1; PID:e1299776; PID:g3261755
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0938

Query Match	100.0%	Score 3993	DB 2	Length 759
Best Local Similarity	100.0%			
Matches	759	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MGSASEQRVLTNA D KVLYPATGTTKSDI F DYYAGVAEVMLGHIA GRPATRKRPNGVDQ	60	
Db	1	MGSASEQRVLTNA D KVLYPATGTTKSDI F DYYAGVAEVMLGHIA GRPATRKRPNGVDQ	60	
Qy	61	PAFFEKQLALSAPP WLSRATVAHRS GTTTYPIDI SATGLWIAQQ AALEHVHP QWRFVAE	120	
Db	61	PAFFEKQLALSAPP WLSRATVAHRS GTTTYPIDI SATGLWIAQQ AALEHVHP QWRFVAE	120	
Qy	121	PGS GELNP GPATR L VF LDL D P GEGV MMA QLAE VARA VRD LLA D I G L V T F P V T S G K G L H L Y	180	
Db	121	PGS GELNP GPATR L VF LDL D P GEGV MMA QLAE VARA VRD LLA D I G L V T F P V T S G K G L H L Y	180	
Qy	181	TPL DEPV SSRG ATV LAK RVA QR L EQ AMP AL V T S MT K S L R A G K V F V D W S Q N G S K T T I A P	240	
Db	181	TPL DEPV SSRG ATV LAK RVA QR L EQ AMP AL V T S MT K S L R A G K V F V D W S Q N G S K T T I A P	240	
Qy	241	YSLRGR THPT VAA PRT WAEL DDP ALR QLS Y D E V L T R I A R D G D L L R E D A P V A D R L T R Y	300	
Db	241	YSLRGR THPT VAA PRT WAEL DDP ALR QLS Y D E V L T R I A R D G D L L R E D A P V A D R L T R Y	300	
Qy	301	RRMRD ASKT PEPI FTAK P V T G D G N T F V I Q E H H A R R P H Y F R L E C D G V L V S W A V P K N L P D N	360	
Db	301	RRMRD ASKT PEPI FTAK P V T G D G N T F V I Q E H H A R R P H Y F R L E C D G V L V S W A V P K N L P D N	360	
Qy	361	TSV NHL LAI TED DH P LEY AT F E G A I P S G E Y G A G K V I I W D S G T Y D T E K F H D D P H T G E V I V N L	420	
Db	361	TSV NHL LAI TED DH P LEY AT F E G A I P S G E Y G A G K V I I W D S G T Y D T E K F H D D P H T G E V I V N L	420	
Qy	421	HGG RIS G Y A L I R T N G D R W L A H R L K N Q K D Q K V F E F D N I A P M L A T H G T V A G L K A S Q W A F E G	480	
Db	421	HGG RIS G Y A L I R T N G D R W L A H R L K N Q K D Q K V F E F D N I A P M L A T H G T V A G L K A S Q W A F E G	480	
Qy	481	KWD GY R L L V E A D H G A V R L R S R G R D V T A E Y P Q L R A L A E D L A D H H V V L D G E A V V L D S S G V P	540	
Db	481	KWD GY R L L V E A D H G A V R L R S R G R D V T A E Y P Q L R A L A E D L A D H H V V L D G E A V V L D S S G V P	540	
Qy	541	SFS QM N R G R D T R V E F W A F D L L Y L D G R A L L G T R Y Q D R R K L L E T L A N A T S L T V P E L P G D	600	

Db 541 SFSQMQNRRDTRVEFWAFDLYLDGRALLGTRYQDRRKLLLETLANATSLTVPELLPGDG 600
Qy 601 AQAFACSRKHGWEGLVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWRAGEGGRSSGV 660
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 AQAFACSRKHGWEGLVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWRAGEGGRSSGV 660
Qy 661 GSLLMGIPGPGLQFAGRVTGLSERELANLKEMLAPLHTDESPFDVPLPARDAKGITYV 720
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 GSLLMGIPGPGLQFAGRVTGLSERELANLKEMLAPLHTDESPFDVPLPARDAKGITYV 720
Qy 721 KPALVAEVRYSEWTPEGRLRQSSWRGLRPDKKPSEVVRE 759
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 721 KPALVAEVRYSEWTPEGRLRQSSWRGLRPDKKPSEVVRE 759